



UTHou-16UTL final.ST25
SEQUENCE LISTING

<110> Board of Regents of the University of Texas System
<120> MUTATIONS IN A NOVEL PHOTORECEPTOR-PINEAL GENE ON 17P CAUSE LEBER
CONGENITAL AMAUROSIS (LCA4)
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<140> 09/765,061
<141> 2001-01-17
<150> 60/331362
<151> 2001-01-14
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<222> (1)..(6689)
<223> The AIPL1 gene produces the aryl-hydrocarbon receptor interacting
protein-like 1

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<222> (1897)..(1906)
<223> n is a, c, g, or t

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UTHou-16UTL final.ST25

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UTHou-16UTL final.ST25

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UTHou-16UTL final.ST25

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UTHou-16UTL final.ST25

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 <213> Papio anubis

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 <222> (1)..(1119)
 <223> The AIPL1 gene produces the aryl-hydrocarbon receptor interacting protein-like 1

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UTHou-16UTL final.ST25

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<212> DNA
<213> Pan troglodytes

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<221> gene
<222> (1)..(1155)
<223> The AIPL1 gene produces the aryl-hydrocarbon receptor interacting protein-like 1

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<212> DNA
<213> Bos taurus

UTHou-16UTL final.ST25

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 <221> gene
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 <223> The AIPL1 gene produces the aryl-hydrocarbon receptor interacting protein-like 1

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<210> 5
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 <212> DNA
 <213> Canis familiaris

<220>
 <221> gene
 <222> (1)..(925)
 <223> The AIPL1 gene produces the aryl-hydrocarbon receptor interacting protein-like 1

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UTHou-16UTL final.ST25

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 <212> DNA
 <213> Mus musculus

<220>
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taccaggagg	ccattgtgtg	cctgaggaac cttcagacca aggagaagcc ctgggaggtt 660

UTHou-16UTL final.ST25

gagtggctga agctggagaa gatgatcaac accctgatcc tcaactactg ccagtgcctg	720
ctgaagaagg aggagtacta cgaggtgttg gagcacacca gcgacattct acgacaccac	780
ccagggatcg tgaaggccta ctatatgcgc gcacgtgctc acgcagaggt gtggaacgct	840
gaggaggcca aggcggacct ggagaaagt ctggagtgtg agccatccat gcgcaaggcg	900
gtgctcaggg aactgcggct gctggagagc cgcctggcgg acaaacagga ggaggagcgg	960
cagcgctgcc ggagcatgct gggctaggct gggctggatt ccactgagtt agactgggtt	1020
aggttgggtg ggagctgcgg gttgaaccct ggggcgaggg ctggggctat ggact	1075

<210> 7
 <211> 1179
 <212> DNA
 <213> Macaca mulatta

<220>
 <221> gene
 <222> (1)..(1179)
 <223> The AIPL1 gene produces the aryl-hydrocarbon receptor interacting protein-like 1

<400> 7	
atggatgccg ctctgctcct gaacgtggaa ggggtcaaga aaaccattct gcacggaggc	60
acgggcgagc tcccaaactt catcaccgga tcccagatga tctttcattt ccgcaccatg	120
aaatgtgatg aggagcgcac ggtcatcgac gacagccgtc aggtggacca gcccatgcac	180
atcatcatcg ggaacatgtt caagctcgag gtctgggaga tcctgctcac ctccatgagg	240
gtgcacgagg tggccgagtt ctggtgcgac accatccaca cgggggtcta ccccatyctg	300
tcccggagcc tgcggcagat ggcccagggc aaggaccca cggagtggca cgtgcacaca	360
tgcgggctgg ccaacatgtt cgcctaccac acgctgggct acgaggacct ggacgagctg	420
cagaaggagc ctacgcctct gatctttgtg atcgagctgc tgcaggttga cgccccgagt	480
gattaccaga gggagacctg gaacctgagc aatcatgaga agatgaaggt ggtgcccgtc	540
ctccacggag agggaaatcg gctcttcaag ytgggccgct acgaggaggc ctcttccaag	600
taccaggagg ccatcatctg cctaaggaac ctgcagacca aggagaagcc gtgggaggtg	660
cagtggctga agctggagaa gatgatcaac accctgaccc tcaactactg ccagtgcctg	720
ctgaagaagg aggagtatta cgaggtgctg gagcacacca gtgacattct ccggcaccac	780
ccaggcatcg tgaaggccta ctatgtcgt gccggggctc acgcggaggt gtggaacgag	840
gccgaggcca aggcggacct ccagaaagt ctggagctgg agccatccat gcagaaggcg	900
gtgcgcaggg agctgaggct gctggagaac cgcattggcg agaagcagga ggaggagagg	960
ctgcgctgcc ggaacatgct gagccagga gccacgcagc ctcccgaga gccaccggca	1020
cagcccccca cagcaccacc tgcagagctg tccacagggc cacctgcgga cccaccggcg	1080

UTHou-16UTL final.ST25

gagcccccca cagcaccacc tgcggagctg tccacagggc cacctgcaga gccacccgca 1140
gagctcccc tgtccccagg gcactcactg cagcactga 1179

<210> 8
<211> 1119
<212> DNA
<213> Saimiri sciureus

<220>
<221> gene
<222> (1)..(1119)
<223> The AIPL1 gene produces the aryl-hydrocarbon receptor interacting protein-like 1

<400> 8
atggatgccg ctctgctcct gaacgtggaa ggggtcaaga agaccattct gcacgggggc 60
acgggcgagc tcccaaattt catcaccgga tcccagagtga tctttcattt ccgcaccatg 120
aaatgtgatg aggagcggac ggtgattgac gacagcaggg aggtgggcca gcccatgcac 180
atcatcatcg ggaacatggt caagctggag gtctgggaga tcctgctcac gtccatgcgg 240
gtgcgagagg tggccgagtt ctggtgagc accatccaca cgggggtcta ccccatcctg 300
tcccggagcc tgcggcagat ggcccagggc aaggaccga cggagtggca tgtgcacacg 360
tgcgggctgg ccaacatggt cgcctaccac acgctgggct acgaggacct ggatgagctg 420
cagaaggagc ctgagcctct gatctttgtg atcgagctgc tgcaggttga tgccccaagt 480
gattaccaga gggagacctg gaacctgagc aatcacgaga agatgaaggt ggtgcccgtc 540
ctccatggag aaggaaatag gctcttcaag ctggggccgct acgaggaggc ctcttccaag 600
taccaggagg ccatcatctg cctaaggaac ctgcagacca aggagaaacc ctgggaggtg 660
cagtggctga agctggagaa gatgatcaat accctgatcc tcaactactg tcagtgtctg 720
ctgaagaagg aggagtacta cgaggtcctg gagcatacca gtgacattct ccggcaccac 780
ccaggcattg tgaaggccta ctatgtgagc gcccgggctc acgcggaggt gtggaacgag 840
gccgaggcca aggcggacct ccagaaagtg ctggagctgg agccgtccat gcagaaggcg 900
gtgagcaggg agctgaggct gctggagaac cgcagtgagg agaagcagga ggaggagcgg 960
ctgagctgcc gcaacatgct gagccagggg gccacgtggt ccccgcgga gccacccgca 1020
gagccacctg cagagtcac cagagagcca cccgagagc cacctgcaga gccacctgca 1080
gagctaacct tgaccccggg gcaccacta cagcactga 1119

<210> 9
<211> 15
<212> DNA
<213> Homo sapiens

UTHou-16UTL final.ST25

<220>
 <221> mutation
 <222> (7)..(9)
 <223> Amino Acid codon position 79: Met to Thr mutation

<400> 9
 acctccacgc ggggtg 15

<210> 10
 <211> 15
 <212> DNA
 <213> Homo sapiens

<220>
 <221> mutation
 <222> (7)..(9)
 <223> Amino Acid condon 88 mutation: Trp to X

<400> 10
 gagttctgat gcgac 15

<210> 11
 <211> 15
 <212> DNA
 <213> Homo sapiens

<220>
 <221> mutation
 <222> (7)..(9)
 <223> Amino Acid condon 96 mutation: Val to Ile mutation

<400> 11
 acggggatct acccc 15

<210> 12
 <211> 15
 <212> DNA
 <213> Homo sapiens

<220>
 <221> mutation
 <222> (7)..(9)
 <223> Amino Acid codon 124 mutation: Thr to Ile mutation

<400> 12
 gaccccatag agtgg 15

<210> 13
 <211> 15
 <212> DNA
 <213> Homo sapiens

<220>
 <221> mutation

UTHou-16UTL final.ST25

<222> (7)..(9)
<223> Amino Acid codon 376 mutation: Pro to Ser mutation

<400> 13
ccaccctcgt cccca

15

<210> 14
<211> 15
<212> DNA
<213> Homo sapiens

<220>
<221> mutation
<222> (7)..(9)
<223> Amino Acid codon 163 mutation: Gln to X mutation

<400> 14
gattactaga gggag

15

<210> 15
<211> 15
<212> DNA
<213> Homo sapiens

<220>
<221> mutation
<222> (7)..(9)
<223> Amino Acid codon 197 mutation: Ala to Pro mutation

<400> 15
gaggagccct cttcc

15

<210> 16
<211> 15
<212> DNA
<213> Homo sapiens

<220>
<221> mutation
<222> (7)..(9)
<223> Amino Acid codon 278 mutation: Trp to X mutation

<400> 16
gaggtgtgaa atgag

15

<210> 17
<211> 15
<212> DNA
<213> Homo sapiens

<220>
<221> mutation
<222> (7)..(7)
<223> a to g mutation: IVS2-2A to G

<400> 17
tccccacggc acacg 15

<210> 18
<211> 15
<212> DNA
<213> Homo sapiens

<220>
<221> mutation
<222> (7)..(9)
<223> Amino Acid codon 262 mutation: Glu to Ser

<400> 18
cacccaagtg cgcgg 15

<210> 19
<211> 15
<212> DNA
<213> Homo sapiens

<220>
<221> mutation
<222> (7)..(9)
<223> Amino Acid codon 302 mutation: Arg to Leu

<400> 19
gcggtgctca gggag 15

<210> 20
<211> 13
<212> DNA
<213> Homo sapiens

<220>
<221> mutation
<222> (5)..(5)
<223> Deletion of "tgcagagccacc" at location 5

<400> 20
gccaccaca gca 13

<210> 21
<211> 15
<212> DNA
<213> Homo sapiens

<220>
<221> mutation
<222> (7)..(9)
<223> Amino Acid codon 239 mutation: Cys to Arg

<400> 21
tgccagcgcc tgctg 15

UTHou-16UTL final.ST25

<210> 22
 <211> 13
 <212> DNA
 <213> Homo sapiens

<220>
 <221> mutation
 <222> (5)..(5)
 <223> two base deletion at location 5: "ag"

<400> 22
 tcccgcagcc acc 13

<210> 23
 <211> 15
 <212> DNA
 <213> Homo sapiens

<220>
 <221> mutation
 <222> (7)..(9)
 <223> Amino Acid codon 42 mutation: Cys to X

<400> 23
 atgaaatgag atgag 15

<210> 24
 <211> 12
 <212> DNA
 <213> Homo sapiens

<220>
 <221> mutation
 <222> (7)..(7)
 <223> nine base deletion at location 7: "ctccggcac"

<400> 24
 gatattcacc ca 12

<210> 25
 <211> 21
 <212> DNA
 <213> Homo sapiens

<220>
 <221> mutation
 <222> (7)..(7)
 <223> eight base insertion: "gtgatctt"

<400> 25
 gactaggtga tcttgtgatc t 21

<210> 26
 <211> 12

<212> DNA
<213> Homo sapiens

<220>
<221> mutation
<222> (4)..(4)
<223> g to a polymorphism: IVS1-9 g to a benign mutation

<400> 26
ctcagtgact ag

12

<210> 27
<211> 12
<212> DNA
<213> Homo sapiens

<220>
<221> mutation
<222> (4)..(4)
<223> g to c polymorphism: IVS2+66G to C Benign

<400> 27
tttgccgggc tg

12

<210> 28
<211> 12
<212> DNA
<213> Homo sapiens

<220>
<221> mutation
<222> (4)..(4)
<223> c to t polymorphism: IVS2-88C to T Benign

<400> 28
tcctctcagg ag

12

<210> 29
<211> 12
<212> DNA
<213> Homo sapiens

<220>
<221> mutation
<222> (4)..(4)
<223> g to a polymorphism: IVS2-14G to A Benign

<400> 29
atccatttat cc

12

<210> 30
<211> 12
<212> DNA
<213> Homo sapiens

<220>
 <221> mutation
 <222> (4)..(4)
 <223> a to c mutation: IVS2-10A to C Benign

<400> 30
 cgtttctccc ca 12

<210> 31
 <211> 12
 <212> DNA
 <213> Homo sapiens

<220>
 <221> mutation
 <222> (4)..(4)
 <223> t to c mutation: IVS3-25T to C Benign

<400> 31
 ctgccccact ga 12

<210> 32
 <211> 12
 <212> DNA
 <213> Homo sapiens

<220>
 <221> mutation
 <222> (7)..(7)
 <223> t to c mutation: IVS3-21T to C Benign

<400> 32
 cctcaccgac ct 12

<210> 33
 <211> 12
 <212> DNA
 <213> Homo sapiens

<220>
 <221> mutation
 <222> (7)..(7)
 <223> g to a mutation: IVS5+18G to A Benign

<400> 33
 aggagcggac ag 12

<210> 34
 <211> 12
 <212> DNA
 <213> Homo sapiens

<220>
 <221> mutation

<222> (7)..(9)
 <223> Amino Acid codon mutation: Asp 90 His Benign

 <400> 34
 tgggtgccaca cc 12

 <210> 35
 <211> 12
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> mutation
 <222> (4)..(6)
 <223> Amino Acid mutation: Phe 37 Phe Benign

 <400> 35
 catttccgca cc 12

 <210> 36
 <211> 12
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> mutation
 <222> (4)..(6)
 <223> Amino Acid mutation: Ser 78 Ser Benign

 <400> 36
 acctctatgc gg 12

 <210> 37
 <211> 12
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> mutation
 <222> (4)..(6)
 <223> Amino Acid mutation: Cys 89 Cys Benign

 <400> 37
 tgggtgtgaca cc 12

 <210> 38
 <211> 12
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> mutation
 <222> (4)..(6)
 <223> Amino Acid codon mutation: Leu 100 Leu Benign

<400> 38
atcctgtccc gg 12

<210> 39
<211> 12
<212> DNA
<213> Homo sapiens

<220>
<221> mutation
<222> (4)..(6)
<223> Amino Acid codon mutation: His 172 His

<400> 39
aatcacgaga ag 12

<210> 40
<211> 12
<212> DNA
<213> Homo sapiens

<220>
<221> mutation
<222> (4)..(6)
<223> Amino Acid codon mutation: Pro 217 Pro Benign

<400> 40
aagccgtggg ag 12

<210> 41
<211> 12
<212> DNA
<213> Homo sapiens

<220>
<221> mutation
<222> (4)..(6)
<223> Amino Acid codon mutation: Asp 255 Asp Benign

<400> 41
agtgacattc tc 12

<210> 42
<211> 20
<212> DNA
<213> Homo sapiens

<220>
<221> primer
<222> (1)..(20)
<223> PCR primer 1 page 57

<400> 42
aagaaaacca ttctgcacgg 20

<210> 43
 <211> 19
 <212> DNA
 <213> Homo sapiens

<220>
 <221> primer
 <222> (1)..(19)
 <223> PCR primer 2 page 57

<400> 43
 tgcagctcgt ccaggtcct 19

<210> 44
 <211> 17
 <212> DNA
 <213> Homo sapiens

<220>
 <221> primer
 <222> (1)..(17)
 <223> PCR primer 1 page 58

<400> 44
 gacacctccc tttctcc 17

<210> 45
 <211> 18
 <212> DNA
 <213> Homo sapiens

<400> 45
 gctggggctg cctggctg 18

<210> 46
 <211> 20
 <212> DNA
 <213> Homo sapiens

<220>
 <221> primer
 <222> (1)..(20)
 <223> PCR primer 3 page 58

<400> 46
 ccgagtgatt accagagga 20

<210> 47
 <211> 20
 <212> DNA
 <213> Homo sapiens

<220>
 <221> primer

<222> (1)..(20)
<223> PCR primer 4 page 58

<400> 47
tgagctccag cacctcatag

20

<210> 48
<211> 18
<212> DNA
<213> Homo sapiens

<220>
<221> primer
<222> (1)..(18)
<223> PCR primer 1 page 60

<400> 48
acgcagaggt gtggaatg

18

<210> 49
<211> 19
<212> DNA
<213> Homo sapiens

<220>
<221> primer
<222> (1)..(19)
<223> PCR primer 2 page 60

<400> 49
aaaaagtgac accacgatc

19

<210> 50
<211> 34
<212> DNA
<213> Homo sapiens

<220>
<221> exon
<222> (1)..(34)
<223> exon - donor splice site 1 of Table 1 page 49
CGGATCCCGAgtgagtggggccctccggagcaga

<400> 50
cgg atc ccg agt gag tgg ggc cct ccg gag cag a
Arg Ile Pro Ser Glu Trp Gly Pro Pro Glu Gln
1 5 10

34

<210> 51
<211> 35
<212> DNA
<213> Homo sapiens

<220>
<221> exon

<222> (1)..(35)

<223> exon - acceptor splice site 1 of Table 1 page 49
cagagtgacacgtctcggtgactagGTGATCTTTC

<400> 51

cag agt gca ccg tct cgg tga cta ggt gat ctt tc
Gln Ser Ala Pro Ser Arg Leu Gly Asp Leu
1 5 10

35

<210> 52

<211> 35

<212> DNA

<213> Homo sapiens

<220>

<221> exon

<222> (1)..(35)

<223> exon - donor splice site 2 of Table 1 page 49

CSACACCATCgtaagtaggccctgcgcgcctgtct

<400> 52

csa cac cat cgt aag tag gcc ctg cgc gcc tgt ct
Xaa His His Arg Lys Ala Leu Arg Ala Cys
1 5 10

35

<210> 53

<211> 35

<212> DNA

<213> Homo sapiens

<220>

<221> exon

<222> (1)..(35)

<223> exon - acceptor splice site 2 of Table 1 page 49

gccatccatccgttttatccccacagCACACGGGGG

<400> 53

gcc atc cat ccg ttt atc ccc aca gca cac ggg gg
Ala Ile His Pro Phe Ile Pro Thr Ala His Gly
1 5 10

35

<210> 54

<211> 35

<212> DNA

<213> Homo sapiens

<220>

<221> exon

<222> (1)..(35)

<223> exon - donor splice site 3 of Table 1 page 49

GCTGCTGCAGgtggggctgggggttggcagggctgg

<400> 54

gct gct gca ggt ggg gct ggg gtt ggc agg gct gg
Page 21

35

Ala Ala Ala Gly Gly Ala Gly Val Gly Arg Ala
1 5 10

<210> 55
<211> 35
<212> DNA
<213> Homo sapiens

<220>
<221> exon
<222> (1)..(35)
<223> exon - acceptor splice site 3 of Table 1 page 49

cactgacctgcagctctggggccagGTTGATGCCC

<400> 55
cac tga cct gca gct ctg ggg cca ggt tga tgc cc 35
His Pro Ala Ala Leu Gly Pro Gly Cys
1 5

<210> 56
<211> 35
<212> DNA
<213> Homo sapiens

<220>
<221> exon
<222> (1)..(35)
<223> exon - donor splice site 4 of Table 1 page 49

GCAGACCAAGgtcagaggccgctggccacggggtg

<400> 56
gca gac caa ggt cag agg ccg ctg gcc acg ggg tg 35
Ala Asp Gln Gly Gln Arg Pro Leu Ala Thr Gly
1 5 10

<210> 57
<211> 35
<212> DNA
<213> Homo sapiens

<220>
<221> exon
<222> (1)..(35)
<223> exon - acceptor splice site 4 of Table 1 page 49

catggctgaccttctccctgggcagGAGAAGCCRT

<400> 57
cat ggc tga cct tct ccc tgg gca gga gaa gcc rt 35
His Gly Pro Ser Pro Trp Ala Gly Glu Ala
1 5 10

<210> 58
<211> 35

<212> DNA
<213> Homo sapiens

<220>
<221> exon
<222> (1)..(35)
<223> exon - donor splice site 5 of Table 1 page 49
CACCACCCAGgtgctgcggggctgcaggggctgcgaca

<400> 58
cac cac cca ggt gcg cgg ggc tgc agg ggc gga ca 35
His His Pro Gly Ala Arg Gly Cys Arg Gly Gly
1 5 10

<210> 59
<211> 35
<212> DNA
<213> Homo sapiens

<220>
<221> exon
<222> (1)..(35)
<223> exon - acceptor splice site 5 of Table 1 page 49
gctggatgctccctgctccccacagGCATCGTGAA

<400> 59
gct gga tgc tcc ctg ctc ccc aca ggc atc gtg aa 35
Ala Gly Cys Ser Leu Leu Pro Thr Gly Ile Val
1 5 10

<210> 60
<211> 18
<212> DNA
<213> Homo sapiens

<220>
<221> primer
<222> (1)..(18)
<223> PCR Primer 1 for AIPL1 fragment amplification Table 5 page 61

<400> 60
ggacacctcc ctttctcc 18

<210> 61
<211> 18
<212> DNA
<213> Homo sapiens

<220>
<221> primer
<222> (1)..(18)
<223> PCR Primer 2 for AIPL1 fragment amplification Table 5 page 61

<400> 61

gctggggctg cctggctg

18

<210> 62
 <211> 20
 <212> DNA
 <213> Homo sapiens

<220>
 <221> primer
 <222> (1)..(20)
 <223> PCR Primer 3 for AIPL1 fragment amplification Table 5 page 61

<400> 62
 ggccttgaa cagtgtgtct

20

<210> 63
 <211> 19
 <212> DNA
 <213> Homo sapiens

<220>
 <221> primer
 <222> (1)..(19)
 <223> PCR Primer 4 for AIPL1 fragment amplification Table 5 page 61

<400> 63
 tttcccgaac cacagcagc

19

<210> 64
 <211> 18
 <212> DNA
 <213> Homo sapiens

<220>
 <221> primer
 <222> (1)..(18)
 <223> PCR Primer 5 for AIPL1 fragment amplification Table 5 page 61

<400> 64
 agtgaggag caggattc

18

<210> 65
 <211> 20
 <212> DNA
 <213> Homo sapiens

<220>
 <221> primer
 <222> (1)..(20)
 <223> PCR Primer 6 for AIPL1 fragment amplification Table 5 page 61

<400> 65
 tgcccatgat gcccgctgtc

20

<210> 66
 <211> 18
 <212> DNA
 <213> Homo sapiens

<220>
 <221> PRIMER
 <222> (1)..(18)
 <223> PCR Primer 7 for AIPL1 fragment amplification Table 5 page 61

<400> 66
 tttcgggtct ctgatggg 18

<210> 67
 <211> 17
 <212> DNA
 <213> Homo sapiens

<220>
 <221> primer
 <222> (1)..(17)
 <223> PCR Primer 8 for AIPL1 fragment amplification Table 5 page 61

<400> 67
 gcaggctccc cagagtc 17

<210> 68
 <211> 19
 <212> DNA
 <213> Homo sapiens

<220>
 <221> primer
 <222> (1)..(19)
 <223> PCR Primer 9 for AIPL1 fragment amplification Table 5 page 61

<400> 68
 gcagctgcct caggtcatg 19

<210> 69
 <211> 18
 <212> DNA
 <213> Homo sapiens

<220>
 <221> primer
 <222> (1)..(18)
 <223> PCR Primer 10 for AIPL1 fragment amplification Table 5 page 61

<400> 69
 gtggggtgga aagaaaag 18

<210> 70
 <211> 18
 <212> DNA

<213> Homo sapiens

<220>

<221> primer

<222> (1)..(18)

<223> PCR Primer 11 for AIPL1 fragment amplification Table 5 page 61

<400> 70

ctgggaaggg agctgtag

18

<210> 71

<211> 19

<212> DNA

<213> Homo sapiens

<220>

<221> primer

<222> (1)..(19)

<223> PCR Primer 12 for AIPL1 fragment amplification Table 5 page 61

<400> 71

aaaagtgaca ccacgatcc

19

<210> 72

<211> 384

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1)..(384)

<223> Human AIPL1 Protein

<220>

<221> misc_feature

<222> (322)..(322)

<223> Xaa can be any naturally occurring amino acid

<400> 72

Met Asp Ala Ala Leu Leu Asn Val Glu Gly Val Lys Lys Thr Ile
1 5 10 15

Leu His Gly Gly Thr Gly Glu Leu Pro Asn Phe Ile Thr Gly Ser Arg
20 25 30

Val Ile Phe His Phe Arg Thr Met Lys Cys Asp Glu Glu Arg Thr Val
35 40 45

Ile Asp Asp Ser Arg Gln Val Gly Gln Pro Met His Ile Ile Ile Gly
50 55 60

Asn Met Phe Lys Leu Glu Val Trp Glu Ile Leu Leu Thr Ser Met Arg
65 70 75 80

UTHou-16UTL final.ST25

Val His Glu Val Ala Glu Phe Trp Cys Asp Thr Ile His Thr Gly Val
85 90 95

Tyr Pro Ile Leu Ser Arg Ser Leu Arg Gln Met Ala Gln Gly Lys Asp
100 105 110

Pro Thr Glu Trp His Val His Thr Cys Gly Leu Ala Asn Met Phe Ala
115 120 125

Tyr His Thr Leu Gly Tyr Glu Asp Leu Asp Glu Leu Gln Lys Glu Pro
130 135 140

Gln Pro Leu Val Phe Val Ile Glu Leu Leu Gln Val Asp Ala Pro Ser
145 150 155 160

Asp Tyr Gln Arg Glu Thr Trp Asn Leu Ser Asn His Glu Lys Met Lys
165 170 175

Ala Val Pro Val Leu His Gly Glu Gly Asn Arg Leu Phe Lys Leu Gly
180 185 190

Arg Tyr Glu Glu Ala Ser Ser Lys Tyr Gln Glu Ala Ile Ile Cys Leu
195 200 205

Arg Asn Leu Gln Thr Lys Glu Lys Pro Trp Glu Val Gln Trp Leu Lys
210 215 220

Leu Glu Lys Met Ile Asn Thr Leu Ile Leu Asn Tyr Cys Gln Cys Leu
225 230 235 240

Leu Lys Lys Glu Glu Tyr Tyr Glu Val Leu Glu His Thr Ser Asp Ile
245 250 255

Leu Arg His His Pro Gly Ile Val Lys Ala Tyr Tyr Val Arg Ala Arg
260 265 270

Ala His Ala Glu Val Trp Asn Glu Ala Glu Ala Lys Ala Asp Leu Gln
275 280 285

Lys Val Leu Glu Leu Glu Pro Ser Met Gln Lys Ala Val Arg Arg Glu
290 295 300

Leu Arg Leu Leu Glu Asn Arg Met Ala Glu Lys Gln Glu Glu Glu Arg
305 310 315 320

Leu Xaa Cys Arg Asn Met Leu Ser Gln Gly Ala Thr Gln Pro Pro Ala

325

335

Glu Pro Pro Thr Glu Pro Pro Ala Gln Ser Ser Thr Glu Pro Pro Ala
340 345 350

Glu Pro Pro Thr Ala Pro Ser Ala Glu Leu Ser Ala Gly Pro Pro Ala
355 360 365

Glu Pro Ala Thr Glu Pro Pro Pro Ser Pro Gly His Ser Leu Gln His
370 375 380

<210> 73
<211> 384
<212> PRT
<213> Pan troglodytes

<220>
<221> Peptide
<222> (1)..(384)
<223> Chimpanzee AIPL1 Protein

<400> 73

Met Asp Ala Ala Leu Leu Leu Asn Val Glu Gly Val Lys Lys Thr Ile
1 5 10 15

Leu His Gly Gly Thr Gly Glu Leu Pro Asn Phe Ile Thr Gly Ser Arg
20 25 30

Val Ile Phe His Phe Arg Thr Met Lys Cys Asp Glu Glu Arg Thr Val
35 40 45

Ile Asp Asp Ser Arg Gln Val Gly Gln Pro Met His Ile Ile Ile Gly
50 55 60

Asn Met Phe Lys Leu Glu Val Trp Glu Ile Leu Leu Thr Ser Met Arg
65 70 75 80

Val His Glu Val Ala Glu Phe Trp Cys Asp Thr Ile His Thr Gly Val
85 90 95

Tyr Pro Ile Leu Ser Arg Ser Leu Arg Gln Met Ala Gln Gly Lys Asp
100 105 110

Pro Thr Glu Trp His Val His Thr Cys Gly Leu Ala Asn Met Phe Ala
115 120 125

Tyr His Thr Leu Gly Tyr Glu Asp Leu Asp Glu Leu Gln Lys Glu Pro
130 135 140

UTHou-16UTL final.ST25

Gln Pro Leu Val Phe Val Ile Glu Leu Leu Gln Val Asp Ala Pro Ser
145 150 155 160

Asp Tyr Gln Arg Glu Thr Trp Asn Leu Ser Asn His Glu Lys Met Lys
165 170 175

Ala Val Pro Val Leu His Gly Glu Gly Asn Arg Leu Phe Lys Leu Gly
180 185 190

Arg Tyr Glu Glu Ala Ser Ser Lys Tyr Gln Glu Ala Ile Ile Cys Leu
195 200 205

Arg Asn Leu Gln Thr Lys Glu Lys Pro Trp Glu Val Gln Trp Leu Lys
210 215 220

Leu Glu Lys Met Ile Asn Thr Leu Ile Leu Asn Tyr Cys Gln Cys Leu
225 230 235 240

Leu Lys Lys Glu Glu Tyr Tyr Glu Val Leu Glu His Thr Ser Asp Ile
245 250 255

Leu Arg His His Pro Gly Ile Val Lys Ala Tyr Tyr Val Arg Ala Arg
260 265 270

Ala His Ala Glu Val Trp Asn Glu Ala Glu Ala Lys Ala Asp Leu Arg
275 280 285

Lys Val Leu Glu Leu Glu Pro Ser Met Gln Lys Ala Val Arg Arg Glu
290 295 300

Leu Arg Leu Leu Glu Asn Arg Met Ala Glu Lys Gln Glu Glu Glu Arg
305 310 315 320

Leu Arg Cys Arg Asn Met Leu Ser Gln Gly Ala Thr Gln Pro Pro Ala
325 330 335

Glu Pro Pro Thr Glu Pro Pro Ala Gln Ser Ser Thr Glu Pro Pro Ala
340 345 350

Glu Pro Pro Pro Ala Pro Ser Ala Glu Leu Ser Ala Gly Pro Pro Ala
355 360 365

Glu Thr Ala Thr Glu Pro Pro Pro Ser Pro Gly His Ser Leu Gln His
370 375 380

<210> 74
<211> 372

UTHou-16UTL final.ST25

<212> PRT
<213> Papio anubis

<220>
<221> peptide
<222> (1)..(372)
<223> Baboon AIPL1 Protein

<400> 74

Met Asp Ala Ala Leu Leu Leu Asn Val Glu Gly Val Lys Lys Thr Ile
1 5 10 15

Leu His Gly Gly Thr Gly Glu Leu Pro Asn Phe Ile Thr Gly Ser Arg
20 25 30

Val Ile Phe His Phe Arg Thr Met Lys Cys Asp Glu Glu Arg Thr Val
35 40 45

Ile Asp Asp Ser Arg Gln Val Asp Gln Pro Met His Ile Ile Ile Gly
50 55 60

Asn Met Phe Lys Leu Glu Val Trp Glu Ile Leu Leu Thr Ser Met Arg
65 70 75 80

Val His Glu Val Ala Glu Phe Trp Cys Asp Thr Ile His Thr Gly Val
85 90 95

Tyr Pro Ile Leu Ser Arg Ser Leu Arg Gln Met Ala Gln Gly Lys Asp
100 105 110

Pro Thr Glu Trp His Val His Thr Cys Gly Leu Ala Asn Met Phe Ala
115 120 125

Tyr His Thr Leu Gly Tyr Glu Asp Leu Asp Glu Leu Gln Lys Glu Pro
130 135 140

Gln Pro Leu Ile Phe Val Ile Glu Leu Leu Gln Val Asp Ala Pro Ser
145 150 155 160

Asp Tyr Gln Arg Glu Thr Trp Asn Leu Ser Asn His Glu Lys Met Lys
165 170 175

Val Val Pro Val Leu His Gly Glu Gly Asn Arg Leu Phe Lys Leu Gly
180 185 190

Arg Tyr Glu Glu Ala Ser Ser Lys Tyr Gln Glu Ala Ile Ile Cys Leu
195 200 205

UTHou-16UTL final.ST25

Arg Asn Leu Gln Thr Lys Glu Lys Pro Trp Glu Val Gln Trp Leu Lys
210 215 220

Leu Glu Lys Met Ile Asn Thr Leu Thr Leu Asn Tyr Cys Gln Cys Leu
225 230 235 240

Leu Lys Lys Glu Glu Tyr Tyr Glu Val Leu Glu His Thr Ser Asp Ile
245 250 255

Leu Arg His His Pro Gly Ile Val Lys Ala Tyr Tyr Val Arg Ala Arg
260 265 270

Ala His Ala Glu Val Trp Asn Glu Ala Glu Ala Lys Ala Asp Leu Gln
275 280 285

Lys Val Leu Glu Leu Glu Pro Ser Met Gln Lys Ala Val Arg Arg Glu
290 295 300

Leu Arg Leu Leu Glu Asn Arg Met Ala Glu Lys Gln Glu Glu Glu Arg
305 310 315 320

Leu Arg Cys Arg Asn Met Leu Ser Gln Gly Ala Thr Gln Pro Pro Thr
325 330 335

Glu Pro Pro Ala Glu Pro His Thr Ala Pro Pro Ala Glu Leu Ser Thr
340 345 350

Gly Pro Pro Ala Glu Pro Pro Ala Glu Leu Pro Leu Ser Pro Gly His
355 360 365

Ser Leu Gln His
370

<210> 75
<211> 328
<212> PRT
<213> Bos taurus

<400> 75

Met Asp Ala Thr Leu Leu Leu Asn Val Glu Gly Ile Lys Lys Thr Ile
1 5 10 15

Leu His Gly Gly Thr Gly Asp Leu Pro Asn Phe Ile Thr Gly Ala Arg
20 25 30

Val Thr Phe His Phe Arg Thr Met Lys Cys Asp Glu Glu Arg Thr Val
35 40 45

UTHou-16UTL final.ST25

Ile Asp Asp Ser Lys Gln Val Gly His Pro Met His Ile Ile Ile Gly
50 55 60

Asn Met Phe Lys Leu Glu Val Trp Glu Ile Leu Leu Thr Ser Met Arg
65 70 75 80

Val Ser Glu Val Ala Glu Phe Trp Cys Asp Thr Ile His Thr Gly Val
85 90 95

Tyr Pro Ile Leu Ser Arg Ser Leu Arg Gln Met Ala Glu Gly Lys Asp
100 105 110

Pro Thr Glu Trp His Val His Thr Cys Gly Leu Ala Asn Met Phe Ala
115 120 125

Tyr His Thr Leu Gly Tyr Glu Asp Leu Asp Glu Leu Gln Lys Glu Pro
130 135 140

Gln Pro Leu Ile Phe Ile Ile Glu Leu Leu Gln Val Glu Ala Pro Ser
145 150 155 160

Gln Tyr Gln Arg Glu Thr Trp Asn Leu Asn Asn Gln Glu Lys Met Gln
165 170 175

Ala Val Pro Ile Leu His Gly Glu Gly Asn Arg Leu Phe Lys Leu Gly
180 185 190

Arg Tyr Glu Glu Ala Ser Asn Lys Tyr Gln Glu Ala Ile Val Cys Leu
195 200 205

Arg Asn Leu Gln Thr Lys Glu Lys Pro Trp Glu Val Gln Trp Leu Lys
210 215 220

Leu Glu Lys Met Ile Asn Thr Leu Ile Leu Asn Tyr Cys Gln Cys Leu
225 230 235 240

Leu Lys Lys Glu Glu Tyr Tyr Glu Val Leu Glu His Thr Ser Asp Ile
245 250 255

Leu Arg His His Pro Gly Ile Val Lys Ala Tyr Tyr Val Arg Ala Arg
260 265 270

Ala His Ala Glu Val Trp Asn Glu Ala Glu Ala Lys Ala Asp Leu Glu
275 280 285

Lys Val Leu Glu Leu Glu Pro Ser Met Arg Lys Ala Val Gln Arg Glu
290 295 300

UTHou-16UTL final.ST25

Leu Arg Leu Leu Glu Asn Arg Leu Glu Glu Lys Arg Glu Glu Glu Arg
305 310 315 320

Leu Arg Cys Arg Asn Met Leu Gly
325

<210> 76
<211> 328
<212> PRT
<213> Mus musculus

<220>
<221> peptide
<222> (1)..(328)
<223> Mouse AIPL1 Protein

<400> 76

Met Asp Val Ser Leu Leu Leu Asn Val Glu Gly Val Lys Lys Thr Ile
1 5 10 15

Leu His Gly Gly Thr Gly Glu Leu Pro Asn Phe Ile Thr Gly Ser Arg
20 25 30

Val Thr Phe His Phe Arg Thr Met Lys Cys Asp Glu Glu Arg Thr Val
35 40 45

Ile Asp Asp Ser Lys Gln Val Gly Gln Pro Met Ser Ile Ile Ile Gly
50 55 60

Asn Met Phe Lys Leu Glu Val Trp Glu Thr Leu Leu Thr Ser Met Arg
65 70 75 80

Leu Gly Glu Val Ala Glu Phe Trp Cys Asp Thr Ile His Thr Gly Val
85 90 95

Tyr Pro Met Leu Ser Arg Ser Leu Arg Gln Val Ala Glu Gly Lys Asp
100 105 110

Pro Thr Ser Trp His Val His Thr Cys Gly Leu Ala Asn Met Phe Ala
115 120 125

Tyr His Thr Leu Gly Tyr Glu Asp Leu Asp Glu Leu Gln Lys Glu Pro
130 135 140

Gln Pro Leu Val Phe Leu Tyr Glu Leu Leu Gln Val Glu Ala Pro Asn
145 150 155 160

Glu Tyr Gln Arg Glu Thr Trp Asn Leu Asn Asn Glu Glu Arg Met Gln

UTHou-16UTL final.ST25

165

170

175

Ala Val Pro Leu Leu His Gly Glu Gly Asn Arg Leu Tyr Lys Leu Gly
180 185 190

Arg Tyr Asp Gln Ala Ala Thr Lys Tyr Gln Glu Ala Ile Val Cys Leu
195 200 205

Arg Asn Leu Gln Thr Lys Glu Lys Pro Trp Glu Val Glu Trp Leu Lys
210 215 220

Leu Glu Lys Met Ile Asn Thr Leu Ile Leu Asn Tyr Cys Gln Cys Leu
225 230 235 240

Leu Lys Lys Glu Glu Tyr Tyr Glu Val Leu Glu His Thr Ser Asp Ile
245 250 255

Leu Arg His His Pro Gly Ile Val Lys Ala Tyr Tyr Met Arg Ala Arg
260 265 270

Ala His Ala Glu Val Trp Asn Ala Glu Glu Ala Lys Ala Asp Leu Glu
275 280 285

Lys Val Leu Glu Leu Glu Pro Ser Met Arg Lys Ala Val Leu Arg Glu
290 295 300

Leu Arg Leu Leu Glu Ser Arg Leu Ala Asp Lys Gln Glu Glu Glu Arg
305 310 315 320

Gln Arg Cys Arg Ser Met Leu Gly
325

<210> 77
<211> 392
<212> PRT
<213> Macaca mulatta

<220>
<221> peptide
<222> (1)..(392)
<223> Rhesus Monkey AILP1 Protein

<400> 77

Met Asp Ala Ala Leu Leu Asn Val Glu Gly Val Lys Lys Thr Ile
1 5 10 15

Leu His Gly Gly Thr Gly Glu Leu Pro Asn Phe Ile Thr Gly Ser Arg
20 25 30

UTHou-16UTL final.ST25

Val Ile Phe His Phe Arg Thr Met Lys Cys Asp Glu Glu Arg Thr Val
35 40 45

Ile Asp Asp Ser Arg Gln Val Asp Gln Pro Met His Ile Ile Ile Gly
50 55 60

Asn Met Phe Lys Leu Glu Val Trp Glu Ile Leu Leu Thr Ser Met Arg
65 70 75 80

Val His Glu Val Ala Glu Phe Trp Cys Asp Thr Ile His Thr Gly Val
85 90 95

Tyr Pro Ile Leu Ser Arg Ser Leu Arg Gln Met Ala Gln Gly Lys Asp
100 105 110

Pro Thr Glu Trp His Val His Thr Cys Gly Leu Ala Asn Met Phe Ala
115 120 125

Tyr His Thr Leu Gly Tyr Glu Asp Leu Asp Glu Leu Gln Lys Glu Pro
130 135 140

Gln Pro Leu Ile Phe Val Ile Glu Leu Leu Gln Val Asp Ala Pro Ser
145 150 155 160

Asp Tyr Gln Arg Glu Thr Trp Asn Leu Ser Asn His Glu Lys Met Lys
165 170 175

Val Val Pro Val Leu His Gly Glu Gly Asn Arg Leu Phe Lys Leu Gly
180 185 190

Arg Tyr Glu Glu Ala Ser Ser Lys Tyr Gln Glu Ala Ile Ile Cys Leu
195 200 205

Arg Asn Leu Gln Thr Lys Glu Lys Pro Trp Glu Val Gln Trp Leu Lys
210 215 220

Leu Glu Lys Met Ile Asn Thr Leu Thr Leu Asn Tyr Cys Gln Cys Leu
225 230 235 240

Leu Lys Lys Glu Glu Tyr Tyr Glu Val Leu Glu His Thr Ser Asp Ile
245 250 255

Leu Arg His His Pro Gly Ile Val Lys Ala Tyr Tyr Val Arg Ala Arg
260 265 270

Ala His Ala Glu Val Trp Asn Glu Ala Glu Ala Lys Ala Asp Leu Gln
275 280 285

UTHou-16UTL final.ST25

Lys Val Leu Glu Leu Glu Pro Ser Met Gln Lys Ala Val Arg Arg Glu
290 295 300

Leu Arg Leu Leu Glu Asn Arg Met Ala Glu Lys Gln Glu Glu Glu Arg
305 310 315 320

Leu Arg Cys Arg Asn Met Leu Ser Gln Gly Ala Thr Gln Pro Pro Ala
325 330 335

Glu Pro Pro Ala Gln Pro Pro Thr Ala Pro Pro Ala Glu Leu Ser Thr
340 345 350

Gly Pro Pro Ala Asp Pro Pro Ala Glu Pro Pro Thr Ala Pro Pro Ala
355 360 365

Glu Leu Ser Thr Gly Pro Pro Ala Glu Pro Pro Ala Glu Leu Pro Leu
370 375 380

Ser Pro Gly His Ser Leu Gln His
385 390

<210> 78
<211> 372
<212> PRT
<213> Saimiri sciureus

<220>
<221> peptide
<222> (1)..(372)
<223> Squirrel Monkey AIPL1 Protein

<400> 78

Met Asp Ala Ala Leu Leu Leu Asn Val Glu Gly Val Lys Lys Thr Ile
1 5 10 15

Leu His Gly Gly Thr Gly Glu Leu Pro Asn Phe Ile Thr Gly Ser Arg
20 25 30

Val Ile Phe His Phe Arg Thr Met Lys Cys Asp Glu Glu Arg Thr Val
35 40 45

Ile Asp Asp Ser Arg Glu Val Gly Gln Pro Met His Ile Ile Ile Gly
50 55 60

Asn Met Phe Lys Leu Glu Val Trp Glu Ile Leu Leu Thr Ser Met Arg
65 70 75 80

UTHou-16UTL final.ST25

Val Arg Glu Val Ala Glu Phe Trp Cys Asp Thr Ile His Thr Gly Val
85 90 95

Tyr Pro Ile Leu Ser Arg Ser Leu Arg Gln Met Ala Gln Gly Lys Asp
100 105 110

Pro Thr Glu Trp His Val His Thr Cys Gly Leu Ala Asn Met Phe Ala
115 120 125

Tyr His Thr Leu Gly Tyr Glu Asp Leu Asp Glu Leu Gln Lys Glu Pro
130 135 140

Gln Pro Leu Ile Phe Val Ile Glu Leu Leu Gln Val Asp Ala Pro Ser
145 150 155 160

Asp Tyr Gln Arg Glu Thr Trp Asn Leu Ser Asn His Glu Lys Met Lys
165 170 175

Val Val Pro Val Leu His Gly Glu Gly Asn Arg Leu Phe Lys Leu Gly
180 185 190

Arg Tyr Glu Glu Ala Ser Ser Lys Tyr Gln Glu Ala Ile Ile Cys Leu
195 200 205

Arg Asn Leu Gln Thr Lys Glu Lys Pro Trp Glu Val Gln Trp Leu Lys
210 215 220

Leu Glu Lys Met Ile Asn Thr Leu Ile Leu Asn Tyr Cys Gln Cys Leu
225 230 235 240

Leu Lys Lys Glu Glu Tyr Tyr Glu Val Leu Glu His Thr Ser Asp Ile
245 250 255

Leu Arg His His Pro Gly Ile Val Lys Ala Tyr Tyr Val Arg Ala Arg
260 265 270

Ala His Ala Glu Val Trp Asn Glu Ala Glu Ala Lys Ala Asp Leu Gln
275 280 285

Lys Val Leu Glu Leu Glu Pro Ser Met Gln Lys Ala Val Arg Arg Glu
290 295 300

Leu Arg Leu Leu Glu Asn Arg Met Ala Glu Lys Gln Glu Glu Glu Arg
305 310 315 320

Leu Arg Cys Arg Asn Met Leu Ser Gln Gly Ala Thr Trp Ser Pro Ala
325 330 335

UTHou-16UTL final.ST25

Glu Pro Pro Ala Glu Pro Pro Ala Glu Ser Ser Thr Glu Pro Pro Ala
 340 345 350

Glu Pro Pro Ala Glu Pro Pro Ala Glu Leu Thr Leu Thr Pro Gly His
 355 360 365

Pro Leu Gln His
 370